# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/553,676A
Source: IFW0
Date Processed by STIC: 10/17/06

# *ENTERED*

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/553,676A

CRF Edit Date: 10/17/06
Edited by: AV

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

_____

___ Moved responses to same line as heading/numeric identifier, specifically:

_____

J Other: Sequence 4- corrected <222> numeric identifier

_____

_____

Revised 09/09/2003

IFWO

**RAW SEQUENCE LISTING** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:56

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

<110> APPLICANT: ASFARI, MARYAM
COFFY, SANDRINE
<120> TITLE OF INVENTION: INSULIN-INDUCED GENE AS THERAPEUTIC TARGET IN DIABETES
<130> FILE REFERENCE: MERCK-3082
<140> CURRENT APPLICATION NUMBER: 10/553,676A
<141> CURRENT FILING DATE: 2005-10-17
<150> PRIOR APPLICATION NUMBER: PCT/EP04/02809
<151> PRIOR FILING DATE: 2004-03-18
<150> PRIOR APPLICATION NUMBER: FR 0304835
<151> PRIOR FILING DATE: 2003-04-17
<160> NUMBER OF SEQ ID NOS: 8
<170> SOFTWARE: PatentIn Ver. 3.3
<210> SEQ ID NO: 1
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Rattus sp.
<400> SEQUENCE: 1

see p.6

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tgtttccctg gctgccagtg tgaggaagag acgtttggcc tctttgacag tttcagcctg 120
atccgagtgg actgcagcag cctgggcccc cacattgtgc ctgtgcccat ccctctggac 180
acagcccacc tggacctgtc ttccaaccgg ctagaaaccg tgaatgagtc agtcctggga 240
gggccaggct ataccacact ggctggcctg gatctcagtc acaacctcct caccagcatc 300
acgcccactg ccttctcccg ccttcgctac ctggagtcac tggacctcag tcacaatggc 360
ctggcagccc tgccagcaga ggttttcacc agctcccccct tgagtgatat caacctgagc 420
cataatcgac ttagagaggt ctcgatatct gccttcacca cccacagcca ggggcgggca 480
ctgcacgtgg acctatccca caatcttatc caccgcctgc tcccctatcc agccagggcc 540
agcctgtccg cacctaccat tcagagcctg aacctgtcct ggaaccggct ccgagccgtg 600
cccgatctcc gagacctacc cctgcgttac ctgagcctgg atgggaaccc tctggctacc 660
atcaacccag gcgccttcat ggggctggcg ggcctcaccc acctttcact ggcaagccta 720
cagggtatcc tccagctacc accccatggc ttccgagagc tcccaggcct tcaggtcctg 780
gacttgtctg gtaaccccaa gctcaagtgg gcaggagccg aggtattttc aggcctgggt 840
ttgctgcaag aactagacct gtctggctcc agcctggtgc ccctgcctga gacgctgcta 900
catcacctcc ctgctttaca gagtgtcagt gtaggccaag atgtgcagtg ccggcgtctg 960
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<210> SEQ ID NO: 2
<211> LENGTH: 353
<212> TYPE: PRT
<213> ORGANISM: Rattus sp.
<400> SEQUENCE: 2

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1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Glu Glu Thr Phe

**RAW SEQUENCE LISTING** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:56

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

```
59                 20                  25                  30
61 Gly Leu Phe Asp Ser Phe Ser Leu Ile Arg Val Asp Cys Ser Ser Leu
62           35                  40                  45
64 Gly Pro His Ile Val Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu
65       50                  55                  60
67 Asp Leu Ser Ser Asn Arg Leu Glu Thr Val Asn Glu Ser Val Leu Gly
68  65                  70                  75                  80
70 Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu
71                  85                  90                  95
73 Leu Thr Ser Ile Thr Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu
74              100                 105                 110
76 Ser Leu Asp Leu Ser His Asn Gly Leu Ala Ala Leu Pro Ala Glu Val
77          115                 120                 125
79 Phe Thr Ser Ser Pro Leu Ser Asp Ile Asn Leu Ser His Asn Arg Leu
80      130                 135                 140
82 Arg Glu Val Ser Ile Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala
83 145                 150                 155                 160
85 Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Leu Pro Tyr
86                  165                 170                 175
88 Pro Ala Arg Ala Ser Leu Ser Ala Pro Thr Ile Gln Ser Leu Asn Leu
89              180                 185                 190
91 Ser Trp Asn Arg Leu Arg Ala Val Pro Asp Leu Arg Asp Leu Pro Leu
92          195                 200                 205
94 Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Thr Ile Asn Pro Gly
95      210                 215                 220
97 Ala Phe Met Gly Leu Ala Gly Leu Thr His Leu Ser Leu Ala Ser Leu
98 225                 230                 235                 240
100 Gln Gly Ile Leu Gln Leu Pro Pro His Gly Phe Arg Glu Leu Pro Gly
101                 245                 250                 255
103 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Lys Trp Ala Gly
104             260                 265                 270
106 Ala Glu Val Phe Ser Gly Leu Gly Leu Leu Gln Glu Leu Asp Leu Ser
107         275                 280                 285
109 Gly Ser Ser Leu Val Pro Leu Pro Glu Thr Leu Leu His His Leu Pro
110     290                 295                 300
112 Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Gln Cys Arg Arg Leu
113 305                 310                 315                 320
115 Val Arg Glu Gly Ala Val His Arg Gln Pro Gly Ser Ser Pro Lys Val
116                 325                 330                 335
118 Val Leu His Cys Gly Asp Thr Gln Glu Ser Ala Arg Gly Pro Asp Ile
119             340                 345                 350
121 Leu
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 2557
127 <212> TYPE: DNA
128 <213> ORGANISM: Homo sapiens
130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (14)..(1072)
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**RAW SEQUENCE LISTING** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:56

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

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133 <223> OTHER INFORMATION: ORF
135 <400> SEQUENCE: 3
136 tccagccccc acc atg ccg tgg ccc ctg ctg ctg ctg gcc gtg agt    49
137                Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser
138                  1               5                  10
140 ggg gcc cag aca acc cgg cca tgc ttc ccc ggg tgc caa tgc gag gtg   97
141 Gly Ala Gln Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val
142          15                  20                  25
144 gag acc ttc ggc ctt ttc gac agc ttc agc ctg act cgg gtg gat tgt   145
145 Glu Thr Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys
146      30                  35                  40
148 agc ggc ctg ggc ccc cac atc atg ccg gtg ccc atc cct ctg gac aca   193
149 Ser Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
150  45                  50                  55                  60
152 gcc cac ttg gac ctg tcc tcc aac cgg ctg gag atg gtg aat gag tcg   241
153 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser
154                  65                  70                  75
156 gtg ttg gcg ggg ccg ggc tac acg acg ttg gct ggc ctg gat ctc agc   289
157 Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser
158              80                  85                  90
160 cac aac ctg ctc acc agc atc tca ccc act gcc ttc tcc cgc ctt cgc   337
161 His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg
162          95                  100                 105
164 tac ctg gag tcg ctt gac ctc agc cac aat ggc ctg rca gcc ctg cca   385
W--> 165 Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro
166      110                 115                 120
168 gcc gag agc ttc acc agc tca ccc ctg agc gac gtg aac ctt agc cac   433
169 Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His
170 125                 130                 135                 140
172 aac cag ctc cgg gag gtc tca gtg tct gcc ttc acg acg cac agt cag   481
173 Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln
174                 145                 150                 155
176 ggc cgg gca cta cac gtg gac ctc tcc cac aac ctc att cac cgc ctc   529
177 Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu
178             160                 165                 170
180 gtg ccc cac ccc acg agg gcc ggc ctg cct gcg ccc acc att cag agc   577
181 Val Pro His Pro Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser
182         175                 180                 185
184 ctg aac ctg gcc tgg aac cgg ctc cat gcc gtg ccc aac ctc cga gac   625
185 Leu Asn Leu Ala Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp
186     190                 195                 200
188 ttg ccc ctg cgc tac ctg agc ctg gat ggg aac cct cta gct gtc att   673
189 Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
190 205                 210                 215                 220
192 ggt ccg ggt gcc ttc gcg ggg ctg gga ggc ctt aca cac ctg tct ctg   721
193 Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
194                 225                 230                 235
196 gcc agc ctg cag agg ctc cct gag ctg gcg ccc agt ggc ttc cgt gag   769
197 Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
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**RAW SEQUENCE LISTING** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:56

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

```
198              240                 245                 250
200 cta ccg ggc ctg cag gtc ctg gac ctg tcg ggc aac ccc aag ctt aac   817
201 Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
202         255                 260                 265
204 tgg gca gga gct gag gtg ttt tca ggc ctg agc tcc ctg cag gag ctg   865
205 Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
206     270                 275                 280
208 gac ctt tcg ggc acc aac ctg gtg ccc ctg cct gag gcg ctg ctc ctc   913
209 Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
210 285                 290                 295                 300
212 cac ctc ccg gca ctg cag agc gtc agc gtg ggc cag gat gtg cgg tgc   961
213 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
214                 305                 310                 315
216 cgg cgc ctg gtg cgg gag ggc acc tac ccc cgg agg cct ggc tcc agc   1009
217 Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
218             320                 325                 330
220 ccc aag gtg gcc ctg cac tgc gta gac acc cgg gaa tct gct gcc agg   1057
221 Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
222         335                 340                 345
224 ggc ccc acc atc ttg tgacaaatgg tgtggcccag ggccacataa cagactgctg   1112
225 Gly Pro Thr Ile Leu
226     350
228 tcctgggctg cctcaggtcc cgagtaactt atgttcaatg tgccaacacc agtggggagc 1172
230 ccgcaggcct atgtggcagc gtcaccacag gagttgtggg cctaggagag gctttggacc 1232
232 tgggagccac acctaggagc aaagtctcac ccctttgtct acgttgcttc cccaaaccat 1292
234 gagcagaggg acttcgatgc caaaccagac tcgggtcccc tcctgcttcc cttccccact 1352
236 tatcccccaa gtgccttccc tcatgcctgg gccggctgac ccgcaatggg cagagggtgg 1412
238 gtggacccct gctgcagggc agagttcagg tccactgggc tgagtgtccc ttgggcccat 1472
240 ggcccagtca ctcaggggcg agtttctttt ctaacatagc cctttctttg ccatgaggcc 1532
242 atgaggcccg cttcatcctt ttctatttcc ctagaacctt aatggtagaa ggaattgcaa 1592
244 agaatcaagt ccacccttct catgtgacag atggggaaac tgaggccttg agaaggaaaa 1652
246 aggctaatct aagttcctgc gggcagtggc atgactggag cacagcctcc tgcctcccag 1712
248 cccggaccca atgcactttc ttgtctcctc taataagccc caccctcccc gcctgggctc 1772
250 cccttgctgc ccttgcctgt tccccattag cacaggagta gcagcagcag gacaggcaag 1832
252 agcctcacaa gtgggactct gggcctctga ccagctgtgc ggcatgggct aagtcactct 1892
254 gcccttcgga gcctctggaa gcttagggca cattggttcc agcctagcca gtttctcacc 1952
256 ctgggttggg gtcccccagc atccagactg gaaacctacc cattttcccc tgagcatcct 2012
258 ctagatgctg ccccaaggag ttgctgcagt tctggagcct catctggctg ggatctccaa 2072
260 ggggcctcct ggattcagtc cccactggcc ctgagcacga cagcccttct taccctccca 2132
262 ggaatgccgt gaaaggagac aaggtctgcc cgacccatgt ctatgctcta ccccagggta 2192
264 gcatctcagc ttccgaaccc tgggctgttt ccttagtctt cattttataa aagttgttgc 2252
266 ctttttaacg gagtgtcact ttcaaccggc ctcccctacc cctgctggcc ggggatggag 2312
268 acatgtcatt tgtaaaagca gaaaaaggtt gcatttgttc acttttgtaa tattgtcctg 2372
270 ggcctgtgtt ggggtgttgg gggaagctgg gcatcagtgg ccacatgggc atcaggggct 2432
272 ggccccacag agaccccaca gggcagtgag ctctgtcttc ccccacctgc ctagcccatc 2492
274 atctatctaa ccggtccttg atttaataaa cactataaaa agttaaaaaa aaaaaaaaaa 2552
276 aaaaa                                                           2557
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 353
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**RAW SEQUENCE LISTING** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:56

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: MOD_RES
286 <222> LOCATION: (121)
287 <223> OTHER INFORMATION: Ala or Thr
289 <400> SEQUENCE: 4

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290 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln Thr
291   1               5                  10                  15
293 Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr Phe Gly
294              20                  25                  30
296 Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser Gly Leu Gly
297          35                  40                  45
299 Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu Asp
300      50                  55                  60
302 Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser Val Leu Ala Gly
303  65                  70                  75                  80
305 Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu Leu
306                  85                  90                  95
308 Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu Ser
309              100                 105                 110
W--> 311 Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro Ala Glu Ser Phe
312          115                 120                 125
314 Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His Asn Gln Leu Arg
315      130                 135                 140
317 Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala Leu
318 145                 150                 155                 160
320 His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Val Pro His Pro
321                 165                 170                 175
323 Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala
324              180                 185                 190
326 Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg
327          195                 200                 205
329 Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala
330      210                 215                 220
332 Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
333 225                 230                 235                 240
335 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly Leu
336                 245                 250                 255
338 Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala Gly Ala
339              260                 265                 270
341 Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp Leu Ser Gly
342          275                 280                 285
344 Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu His Leu Pro Ala
345      290                 295                 300
347 Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys Arg Arg Leu Val
348 305                 310                 315                 320
350 Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser Pro Lys Val Ala
351                 325                 330                 335
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**RAW SEQUENCE LISTING ERROR SUMMARY** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:57

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

**Please Note:**
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; Xaa Pos. 121
Seq#:4; Xaa Pos. 121

**VERIFICATION SUMMARY** DATE: 10/17/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 15:03:57

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\10172006\J553676A.raw**

L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:385
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:112

# Raw Sequence Listing before editing (for reference only)

IFWO

**RAW SEQUENCE LISTING** DATE: 10/16/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 08:48:10

Input Set : **A:\MERC3082.APP**
Output Set: **N:\CRF4\10162006\J553676A.raw**

<110> APPLICANT: ASFARI, MARYAM
COFFY, SANDRINE
<120> TITLE OF INVENTION: INSULIN-INDUCED GENE AS THERAPEUTIC TARGET IN DIABETES
<130> FILE REFERENCE: MERCK-3082
<140> CURRENT APPLICATION NUMBER: 10/553,676A
<141> CURRENT FILING DATE: 2005-10-17
<150> PRIOR APPLICATION NUMBER: PCT/EP04/02809
<151> PRIOR FILING DATE: 2004-03-18
<150> PRIOR APPLICATION NUMBER: FR 0304835
<151> PRIOR FILING DATE: 2003-04-17
<160> NUMBER OF SEQ ID NOS: 8
<170> SOFTWARE: PatentIn Ver. 3.3
<210> SEQ ID NO: 1
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Rattus sp.
<400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed

atgttgtgca ccctgttcct gctactgctg gccctgggca tagtgcagac aactcggcca 60
tgtttccctg gctgccagtg tgaggaagag acgtttggcc tctttgacag tttcagcctg 120
atccgagtgg actgcagcag cctgggcccc cacattgtgc ctgtgcccat ccctctggac 180
acagcccacc tggacctgtc ttccaaccgg ctagaaaccg tgaatgagtc agtcctggga 240
gggccaggct ataccacact ggctggcctg gatctcagtc acaacctcct caccagcatc 300
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cataatcgac ttagagaggt ctcgatatct gccttcacca cccacagcca ggggcgggca 480
ctgcacgtgg acctatccca caatcttatc caccgcctgc tcccctatcc agccagggcc 540
agcctgtccg cacctaccat tcagagcctg aacctgtcct ggaaccggct ccgagccgtg 600
cccgatctcc gagacctacc cctgcgttac ctgagcctgg atgggaaccc tctggctacc 660
atcaacccag gcgccttcat ggggctggcg ggcctcaccc acctttcact ggcaagccta 720
cagggtatcc tccagctacc accccatggc ttccgagagc tcccaggcct tcaggtcctg 780
gacttgtctg gtaaccccaa gctcaagtgg gcaggagccg aggtattttc aggcctgggt 840
ttgctgcaag aactagacct gtctggctcc agcctggtgc ccctgcctga gacgctgcta 900
catcacctcc ctgctttaca gagtgtcagt gtaggccaag atgtgcagtg ccggcgtctg 960
gtacgggagg gtgcctacca ccgccaaccc ggttccagcc ctaaggtagt cctgcactgt 1020
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<210> SEQ ID NO: 2
<211> LENGTH: 353
<212> TYPE: PRT
<213> ORGANISM: Rattus sp.
<400> SEQUENCE: 2

Met Leu Cys Thr Leu Phe Leu Leu Leu Leu Ala Leu Gly Ile Val Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Glu Glu Thr Phe

**RAW SEQUENCE LISTING** DATE: 10/16/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 08:48:10

Input Set : **A:\MERC3082.APP**
Output Set: **N:\CRF4\10162006\J553676A.raw**

```
59                 20                  25                  30
61 Gly Leu Phe Asp Ser Phe Ser Leu Ile Arg Val Asp Cys Ser Ser Leu
62           35                  40                  45
64 Gly Pro His Ile Val Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu
65       50                  55                  60
67 Asp Leu Ser Ser Asn Arg Leu Glu Thr Val Asn Glu Ser Val Leu Gly
68   65                  70                  75                  80
70 Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu
71                   85                  90                  95
73 Leu Thr Ser Ile Thr Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu
74               100                 105                 110
76 Ser Leu Asp Leu Ser His Asn Gly Leu Ala Ala Leu Pro Ala Glu Val
77           115                 120                 125
79 Phe Thr Ser Ser Pro Leu Ser Asp Ile Asn Leu Ser His Asn Arg Leu
80       130                 135                 140
82 Arg Glu Val Ser Ile Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala
83 145                 150                 155                 160
85 Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Leu Pro Tyr
86                   165                 170                 175
88 Pro Ala Arg Ala Ser Leu Ser Ala Pro Thr Ile Gln Ser Leu Asn Leu
89               180                 185                 190
91 Ser Trp Asn Arg Leu Arg Ala Val Pro Asp Leu Arg Asp Leu Pro Leu
92           195                 200                 205
94 Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Thr Ile Asn Pro Gly
95       210                 215                 220
97 Ala Phe Met Gly Leu Ala Gly Leu Thr His Leu Ser Leu Ala Ser Leu
98 225                 230                 235                 240
100 Gln Gly Ile Leu Gln Leu Pro Pro His Gly Phe Arg Glu Leu Pro Gly
101                  245                 250                 255
103 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Lys Trp Ala Gly
104              260                 265                 270
106 Ala Glu Val Phe Ser Gly Leu Gly Leu Leu Gln Glu Leu Asp Leu Ser
107          275                 280                 285
109 Gly Ser Ser Leu Val Pro Leu Pro Glu Thr Leu Leu His His Leu Pro
110      290                 295                 300
112 Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Gln Cys Arg Arg Leu
113 305                 310                 315                 320
115 Val Arg Glu Gly Ala Val His Arg Gln Pro Gly Ser Ser Pro Lys Val
116                  325                 330                 335
118 Val Leu His Cys Gly Asp Thr Gln Glu Ser Ala Arg Gly Pro Asp Ile
119              340                 345                 350
121 Leu
125 <210> SEQ ID NO: 3
126 <211> LENGTH: 2557
127 <212> TYPE: DNA
128 <213> ORGANISM: Homo sapiens
130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (14)..(1072)
```

**RAW SEQUENCE LISTING** DATE: 10/16/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 08:48:10

Input Set : **A:\MERC3082.APP**
Output Set: **N:\CRF4\10162006\J553676A.raw**

```
133 <223> OTHER INFORMATION: ORF
135 <400> SEQUENCE: 3
136 tccagccccc acc atg ccg tgg ccc ctg ctg ctg ctg ctg gcc gtg agt    49
137                Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser
138                  1               5                  10
140 ggg gcc cag aca acc cgg cca tgc ttc ccc ggg tgc caa tgc gag gtg   97
141 Gly Ala Gln Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val
142          15                  20                  25
144 gag acc ttc ggc ctt ttc gac agc ttc agc ctg act cgg gtg gat tgt   145
145 Glu Thr Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys
146      30                  35                  40
148 agc ggc ctg ggc ccc cac atc atg ccg gtg ccc atc cct ctg gac aca   193
149 Ser Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
150  45                  50                  55                  60
152 gcc cac ttg gac ctg tcc tcc aac cgg ctg gag atg gtg aat gag tcg   241
153 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser
154                  65                  70                  75
156 gtg ttg gcg ggg ccg ggc tac acg acg ttg gct ggc ctg gat ctc agc   289
157 Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser
158              80                  85                  90
160 cac aac ctg ctc acc agc atc tca ccc act gcc ttc tcc cgc ctt cgc   337
161 His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg
162          95                  100                 105
164 tac ctg gag tcg ctt gac ctc agc cac aat ggc ctg rca gcc ctg cca   385
W--> 165 Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro
166      110                 115                 120
168 gcc gag agc ttc acc agc tca ccc ctg agc gac gtg aac ctt agc cac   433
169 Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His
170 125                 130                 135                 140
172 aac cag ctc cgg gag gtc tca gtg tct gcc ttc acg acg cac agt cag   481
173 Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln
174                 145                 150                 155
176 ggc cgg gca cta cac gtg gac ctc tcc cac aac ctc att cac cgc ctc   529
177 Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ile His Arg Leu
178             160                 165                 170
180 gtg ccc cac ccc acg agg gcc ggc ctg cct gcg ccc acc att cag agc   577
181 Val Pro His Pro Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser
182         175                 180                 185
184 ctg aac ctg gcc tgg aac cgg ctc cat gcc gtg ccc aac ctc cga gac   625
185 Leu Asn Leu Ala Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp
186     190                 195                 200
188 ttg ccc ctg cgc tac ctg agc ctg gat ggg aac cct cta gct gtc att   673
189 Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
190 205                 210                 215                 220
192 ggt ccg ggt gcc ttc gcg ggg ctg gga ggc ctt aca cac ctg tct ctg   721
193 Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
194                 225                 230                 235
196 gcc agc ctg cag agg ctc cct gag ctg gcg ccc agt ggc ttc cgt gag   769
197 Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
```

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198             240                 245                 250
200 cta ccg ggc ctg cag gtc ctg gac ctg tcg ggc aac ccc aag ctt aac   817
201 Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
202         255                 260                 265
204 tgg gca gga gct gag gtg ttt tca ggc ctg agc tcc ctg cag gag ctg   865
205 Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
206     270                 275                 280
208 gac ctt tcg ggc acc aac ctg gtg ccc ctg cct gag gcg ctg ctc ctc   913
209 Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
210 285                 290                 295                 300
212 cac ctc ccg gca ctg cag agc gtc agc gtg ggc cag gat gtg cgg tgc   961
213 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
214                 305                 310                 315
216 cgg cgc ctg gtg cgg gag ggc acc tac ccc cgg agg cct ggc tcc agc   1009
217 Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
218             320                 325                 330
220 ccc aag gtg gcc ctg cac tgc gta gac acc cgg gaa tct gct gcc agg   1057
221 Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
222         335                 340                 345
224 ggc ccc acc atc ttg tgacaaatgg tgtggcccag ggccacataa cagactgctg   1112
225 Gly Pro Thr Ile Leu
226     350
228 tcctgggctg cctcaggtcc cgagtaactt atgttcaatg tgccaacacc agtggggagc 1172
230 ccgcaggcct atgtggcagc gtcaccacag gagttgtggg cctaggagag gctttggacc 1232
232 tgggagccac acctaggagc aaagtctcac ccctttgtct acgttgcttc cccaaaccat 1292
234 gagcagaggg acttcgatgc caaaccagac tcgggtcccc tcctgcttcc cttccccact 1352
236 tatcccccaa gtgccttccc tcatgcctgg gccggctgac ccgcaatggg cagagggtgg 1412
238 gtggacccct gctgcagggc agagttcagg tccactgggc tgagtgtccc ttgggcccat 1472
240 ggcccagtca ctcaggggcg agtttctttt ctaacatagc cctttctttg ccatgaggcc 1532
242 atgaggcccg cttcatcctt ttctatttcc ctagaacctt aatggtagaa ggaattgcaa 1592
244 agaatcaagt ccacccttct catgtgacag atggggaaac tgaggccttg agaaggaaaa 1652
246 aggctaatct aagttcctgc gggcagtggc atgactggag cacagcctcc tgcctcccag 1712
248 cccggaccca atgcactttc ttgtctcctc taataagccc caccctcccc gcctgggctc 1772
250 cccttgctgc ccttgcctgt tccccattag cacaggagta gcagcagcag gacaggcaag 1832
252 agcctcacaa gtgggactct gggcctctga ccagctgtgc ggcatgggct aagtcactct 1892
254 gcccttcgga gcctctggaa gcttagggca cattggttcc agcctagcca gtttctcacc 1952
256 ctgggttggg gtcccccagc atccagactg gaaacctacc cattttcccc tgagcatcct 2012
258 ctagatgctg ccccaaggag ttgctgcagt tctggagcct catctggctg ggatctccaa 2072
260 ggggcctcct ggattcagtc cccactggcc ctgagcacga cagcccttct taccctccca 2132
262 ggaatgccgt gaaaggagac aaggtctgcc cgacccatgt ctatgctcta ccccagggta 2192
264 gcatctcagc ttccgaaccc tgggctgttt ccttagtctt cattttataa aagttgttgc 2252
266 ctttttaacg gagtgtcact ttcaaccggc ctcccctacc cctgctggcc ggggatggag 2312
268 acatgtcatt tgtaaaagca gaaaaaggtt gcatttgttc acttttgtaa tattgtcctg 2372
270 ggcctgtgtt ggggtgttgg gggaagctgg gcatcagtgg ccacatgggc atcaggggct 2432
272 ggccccacag agaccccaca gggcagtgag ctctgtcttc ccccacctgc ctagcccatc 2492
274 atctatctaa ccggtccttg atttaataaa cactataaaa agttaaaaaa aaaaaaaaaa 2552
276 aaaaa                                                           2557
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 353
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Input Set : A:\MERC3082.APP
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insert opening bracket

281 <212> TYPE: PRT
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: MOD_RES
286 <222> LOCATION: 222> (121)
287 <223> OTHER INFORMATION: Ala or Thr
289 <400> SEQUENCE: 4

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290 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln Thr
291   1               5                  10                  15
293 Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr Phe Gly
294              20                  25                  30
296 Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser Gly Leu Gly
297          35                  40                  45
299 Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr Ala His Leu Asp
300      50                  55                  60
302 Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu Ser Val Leu Ala Gly
303  65                  70                  75                  80
305 Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu Ser His Asn Leu Leu
306                  85                  90                  95
308 Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu Arg Tyr Leu Glu Ser
309              100                 105                 110
W--> 311 Leu Asp Leu Ser His Asn Gly Leu Xaa Ala Leu Pro Ala Glu Ser Phe
312          115                 120                 125
314 Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser His Asn Gln Leu Arg
315      130                 135                 140
317 Glu Val Ser Val Ser Ala Phe Thr Thr His Ser Gln Gly Arg Ala Leu
318 145                 150                 155                 160
320 His Val Asp Leu Ser His Asn Leu Ile His Arg Leu Val Pro His Pro
321                  165                 170                 175
323 Thr Arg Ala Gly Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala
324              180                 185                 190
326 Trp Asn Arg Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg
327          195                 200                 205
329 Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala
330      210                 215                 220
332 Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
333 225                 230                 235                 240
335 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly Leu
336                  245                 250                 255
338 Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala Gly Ala
339              260                 265                 270
341 Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp Leu Ser Gly
342          275                 280                 285
344 Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu His Leu Pro Ala
345      290                 295                 300
347 Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys Arg Arg Leu Val
348 305                 310                 315                 320
350 Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser Pro Lys Val Ala
351                  325                 330                 335
```

**RAW SEQUENCE LISTING ERROR SUMMARY** DATE: 10/16/2006
PATENT APPLICATION: **US/10/553,676A** TIME: 08:48:11

Input Set : **A:\MERC3082.APP**
Output Set: **N:\CRF4\10162006\J553676A.raw**

**Please Note:**
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; Xaa Pos. 121
Seq#:4; Xaa Pos. 121

**VERIFICATION SUMMARY** DATE: 10/16/2006
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Input Set : **A:\MERC3082.APP**
Output Set: **N:\CRF4\10162006\J553676A.raw**

L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:385
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:112